Abstract

Captive breeding has become a critical tool for the restoration of amphibian populations decimated by diseases. However, much is unknown about effects of long-term captivity on amphibian health and particularly immune system function. Therefore, we have begun a project to understand the effects of captivity and captive breeding on the cutaneous microbiome of lungless salamanders. The community of microbes living in and on the skin of lungless salamanders (Plethodontidae) is an important predictor of the organisms' ability to ward off diseases like chytridiomycosis. We compare the microbiome of wild and long-term (8 years) captive or captive-bred Ocoee and Blue Ridge two-lined salamanders (Desmognathus ocoee and Eurycea wilderae, respectively) all from the Charles H. Wharton Conservation Center in Union County, GA. Microbiome communities were estimated by amplifying the V4 region of the 16S rDNA gene and then comparing with sequences from the Greengenes database. We present our study design and preliminary results.